Please amend the paragraph commencing at page 2, line 19 to read as follows:

Figure 3 shows a 1069 bp DNA sequence (SEQ ID NO:18) comprising the *Lunaria annua FAE1* transcription regulatory sequence.

Please amend the partial paragraph at page 2, lines 21-33 to read as follows:

Figure 4 shows an alignment of the *Arabidopsis thaliana (A.t.)* (SEQ ID NO:19), *Lunaria annua (L.a.)* (SEQ ID NO:21) and *Brassica napus (B.n.)* (SEQ ID NO:20) transcription regulatory sequences. Asterisks below the sequences indicate identical nucleotides in each of the three sequences. A number of putative cis-acting sequence motifs are identified in the *A. thaliana* sequence: an EMl ABA box at -44bp to -36bp having the sequence ACATCTCAT, for which the published consensus sequence is ACGTGTCAT (Rowley, D.L. and Herman, E.M. (1997), Biochimica et Biophysica Acta 1345:1-4); an A-300 box at -51bp to -46bp having the sequence TGCAAT, for which the published consensus sequence is TG(T/A/C)AAA(G/T) (Morton et al. (1994) in Seed Development and Germination (Kigel, J. and Gallili, G., eds.) pp. 103-138, Marcel Dekker, New York); G-box 1 at -105 to -100 bp having the sequence CACATG, for which is the consensus sequence is CACCTG, and G-box 2 at -164 to -159 bp having the sequence CAACTT, for which the consensus sequence is CAACTG (Kawogoe, Y. and Murai, N. (1992) Plant J. 2:927-936; CEl element at -226 to -218 bp having the sequence

Please amend the partial paragraph at page 3, lines 1-9 to read as follows:

TTCCATCGA, for which the consensus sequence is TGCCACCGG, and a CE3 element at -381 bp to -369 bp having the sequence ACACATTCCCTC (SEQ ID NO:1), for which the consensus sequence is ACGCGTGTCCTC (SEQ ID NO:2) (Shen et al., (1996) Plant Cell 8:1107-1119). Not highlighted is a putative RY repeat motif at -53bp to -47bp having the sequence CATGCAA, for which the consensus sequence is CATGCAT (Dickinson et al. (1988) Nucleic Acid Res. 16:371; Lelievre et al. (1992) Plant Physiol. 98:387-391). Also shown, as Con. 4, is a consensus sequence (SEQ ID NO:22), wherein R=G or A, Y=T/U or C, M=A or C, K=G or T/U, S=G or C, W=A or T/U, B=G or C or T/U, D=A or G or T/U, H=A or C or T/U, V=A or G or C and N=A or G or C or T/U.

Please amend the paragraph commencing at page 3, line 10 to read as follows:

Figure 5 shows an alignment of the *Arabidopsis thaliana (A.t.)* and *Lunaria annua (L.a.)* transcription regulatory sequences. Asterisks below the sequences indicate identical nucldectides in each of the two sequences. The base at position -400 in the *A.t.* sequence is highlighted. The alignment of sequences in both Figure 4 and Figure 5 was accomplished using the CLUSTALW program (version 1.74) for multiple sequence alignments, using a gap open penalty of 15, a gap extension penalty of 6.66 and an IUB DNA weight matrix. Also shown, as Con. 5, is a consensus sequence (SEQ ID NO:23), wherein R=G or A, Y=T/U or C, M=A or C, K=G or T/U, S=G or C, W=A or T/U, B=G or C or T/U, D=A or G or T/U, H=A or C or T/U, V=A or G or C and N=A or G or C or T/U.

Please amend the partial paragraph at page 7, lines 1-33 to read as follows:

Optimal alignment of sequences for comparisons of similarity may be automated using a variety of algorithms, such as the local homology algorithm of Smith and Waterman (1981) *Adv. Appl. Math* 2:482, the homology alignment algorithm of Needleman and Wunsch (1970) *J. Mol. Biol.* 48:443, the search for similarity method of Pearson and Lipman (1988) *Proc. Natl. Acad. Sci. USA* 85:2444, and the computerized implementations of these algorithms (such as GAP, BESTFIT, FASTA and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, Madison, WI, U.S.A.). sequence similarity may also be determined using the BLAST algorithm, described in Altschul *et al.* (1990), *J. Mol. Biol.* 215:403-10 (using the published default settings). Software and instructions for performing BLAST analysis may be available through the National Center for Biotechnology Information in the United States (including the programs BLASTP, BLASTN, BLASTX, TBLASTN and TBLASTX that may be available through the internet at www.ncbi.nlm.nih.gov/. The BLAST algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence that either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database (reference) sequence. T is referred to as the neighborhood word score threshold. Initial neighborhood word hits act as seeds for initiating searches to find longer HSPs. The word hits are extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Extension of the word hits in each direction is halted when the following parameters are met: the cumulative alignment score falls

off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T and X determine the sensitivity and speed of the alignment. The BLAST program may use as defaults a word length (W) of 11, the BLOSUM62 scoring matrix (Henikoff and Henikoff (1992) *Proc. Natl. Acad. Sci. USA* 89:10915-10919), a gap existence cost of 11, a per residue gap cost of 1, a lambda ratio of 0.85, alignments (B) of 50, expectation (E) of 10, M=5, N=4, and a comparison of both strands. One measure of the statistical similarity between two sequences using the BLAST algorithm is the smallest sum probability (P(N)), which provides an indication of the probability by which a match between two nucleotide or amino acid sequences would occur by chance. In alternative embodiments of the invention, nucleotide or amino acid sequences are considered substantially identical if the smallest sum probability in a comparison of the test sequences is less than about 1, preferably less than about 0.1, more preferably less than

Please amend the paragraph commencing at page 12, line 1 to read as follows:

Using the sequence information of the *A. thaliana* genome sequencing project, synthetic oligonucleotide primers were designed to amplify the *FAE1* 5' untranslated region, to isolate it by PCR. As shown in Figure 1, the upstream primer 5'-CTAGTAGATTGGTTGGTTGGTTTCC-3' (AtproFW) (SEQ ID NO:3) in combination with the downstream primer 5'-TGCTCTGTTTGTGTCGGAAAATAATGG-3' (AtproRV) (SEQ ID NO:4) were used, and resulted in the synthesis of a fragment of the correct size (934 bp). The amplified product was subcloned in the *Hin*cII site of the plasmid pT7T3-18U (Pharmacia) to produce plasmid pT7T3-18U/proFAE900, followed by complete sequence determination of both strands to verify the fragment identity. A BLAST search of the *A. thaliana* Database identified a single BAC clone T4L20 (GenBank ATF10M6) 125,179 bp long, which contains the complete *FAE1* gene.

Please amend the partial paragraph at page 12, lines 18-32 to read as follows:

Construction of the vectors pFAE900-GUS and pFAE400-GUS, and transformation of *Arabidopsis* and tobacco, was as follows. The insert was cleaved out of pT7T3-18U vector with *Hin*dIII and *Xba*I and directionally subcloned into the corresponding sites of the binary Ti

plasmid pBI101 (Clontech), which contains a promoterless GUS gene (Jefferson et al. 1987), to obtain the vector pFAE900-GUS. Another construct, pFAE400-GUS, containing only 393 bp of the 5' *FAE1* region directly upstream of the ATG initiation codon (SEQ ID NO:15) fused to the GUS coding sequence was also generated. For that, the pT7T3-18U/proFAE900 vector was digested with *BglII* and *PstI*, the sticky ends were filled in using T4 DNA polymerase, followed by re-ligation to obtain pT7T3-18U/proFAE400. The 393 bp 5' *FAE1* upstream fragment was then excised with *Hin*dIII and *Xba*I and cloned into the binary vector pBI101 to obtain the plasmid pFAE400-GUS. The pFAE400-GUS and pFAE900-GUS fusion constructs in pBI101 were introduced into *Agrobacterium tumefaciens* strain GV3101 (Koncz and Schell, 1986) by heat-shock and selected for resistance to kanamycin (50 μg/ml). *A. thaliana* (L.) Heynh. ecotype Columbia was transformed with the pFAE400-GUS and pFAE900-GUS constructs using floral dip method (Clough and Bent, 1998). Screening for transformed seed

Please amend the partial paragraph at page 15, lines 1-10 to read as follows:

cutting restriction enzymes (*DraI, EcoRV, HpII, PvuII and ScaI*) to generate a series of DNA libraries. After ligation of adapter molecules, individual libraries were used as templates in a two step PCR. In the first PCR amplification using the AP1 primer 5'-GGATCCTAATACGACTCACTATAGGGC-3' (SEQ ID NO:5) and the *FAE1* gene specific primer 5'-AAAGAGTGGAGCGATGGTTATGAGG-3' (SEQ ID NO:6) (Bnwalk1), multiple DNA fragments were amplified from all five library templates. After a second round of PCR, using the AP2 primer 5'-CTATAGGGCTCGAGCGGC-3' (SEQ ID NO:7) and the nested *FAE1* specific primer 5'-CGGAAAGAAGCAAAGGTTGAAAAGG-3' (SEQ ID NO:8) (Bnwalk2), the longest single fragment of 1.6 kb was obtained from the *HpaI* library template. This fragment was inserted into the pCR2.1 plasmid (Invitrogen) and sequenced. The sequence is shown in Figure 2.

Please amend the paragraph at page 15, line 11 to read as follows:

For the PCR walking experiment to isolate the *L. annua* 5' regulatory region, in addition to the standard APl and AP2 primers, the following *FAE1* specific primers were used: 5'-GATCGTTTGTGGTAAGACGAGAGC-3' (SEQ ID NO:9) (Lawalk1) and 5'-GTCAGTGGGAAGAAACAGAGGTTG-3' (SEQ ID NO:10) (Lawalk2). In the first PCR

reaction, the *DraI, EcoRV, PvuII, ScaI* and *SspI* library templates were used. In a second PCR amplification the longest single fragment 1.1 kb in length was synthesized using the *EcoRV* library template. This fragment was inserted into the *HincII* site of the pT7T3-18U vector (Promega), sequenced on both strands and analyzed (Figure 3).

Please amend the paragraph at page 15, line 19 to read as follows:

Using the sequence data obtained for the 5' regulatory regions generated by PCR walking, specific primers were generated for the amplification of the *L. annua* and *B. napus FAE1* promoter fragments. For the PCR-amplification of *B. napus* promoter fragment the upstream primer was 5'-CTGACTTCACCAAAGAAACAACTCG-3' (SEQ ID NO:11) (BnproFW) in combination with the downstream primer 5'-CGGAATTCCGTTTTTTTTTTAGGCG-3' (SEQ ID NO:12) (BnproRV). The synthesized fragment was ligated into the *SmaI* site of pGEM-7Zf (Promega), then excised with *XbaI/BamHI* and cloned into the equivalent sites of the pBI101 binary vector (Clontech). *L. annua* 5' regulatory region was amplified using the 5'-CAGCTTAACCGGTAAAATTGGCC-3' (SEQ ID NO:13) (LaproFW) upstream primer together with the 5'-TGTTCAGTTTTGTGTCGGAGAGG-3' (SEQ ID NO:14) (LaproRV) downstream primer and inserted in the *HincII* site of pT7T3-18U (Promega) plasmid. In order to clone the *L. annua* promter fragment into the pBI101 binary vector, an *XbaI* site was added by subcloning the *PstI/KpnI* fragment released from the pT7T3-18U vector into pBluescript II KS+ (Stratagene). The fragment was then excised and cloned in the *XbaI* site of the pBI101 vector.

In the Claims:

Please add new claims 29-38, and amend claims 1 and 19 to read as follows:

1. (Amended twice) A recombinant nucleic acid molecule comprising a heterologous promoter sequence operably linked to a nucleic acid sequence, wherein the promoter sequence comprises a transcriptional regulatory region capable of directing seed-specific expression in *Arabidopsis* wherein the transcriptional regulatory region hybridizes under stringent conditions to a sequence selected from the group consisting of SEQ ID NO:15, 16 , 17, and 18, or the complement thereof.